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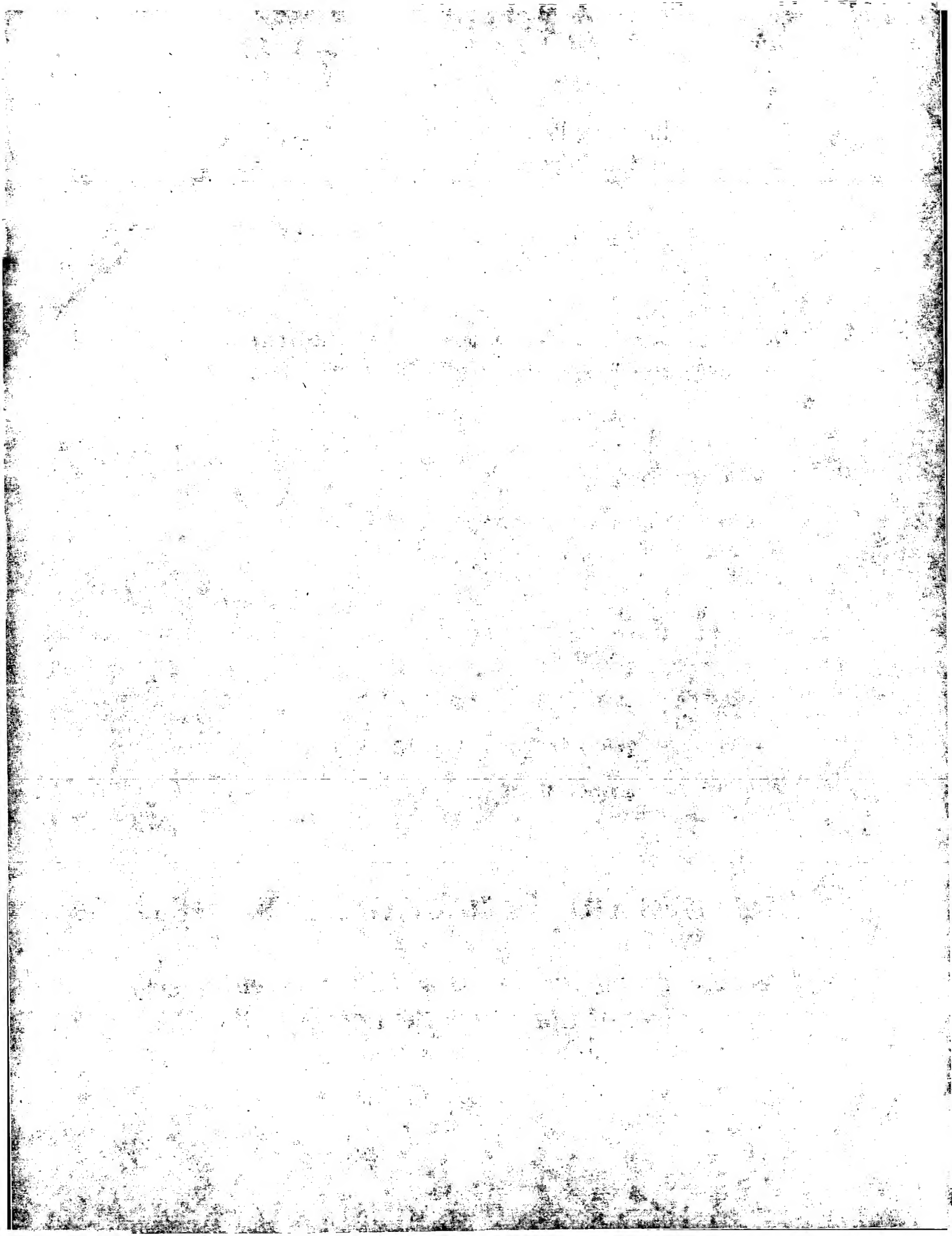
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(54) Title: METHOD FOR ASSAYING PROTEOLYTIC ENZYMES USING FLUORESCENCE-QUENCHED SUBSTRATES		
(57) Abstract <p>A method is disclosed for assaying a proteolytic enzyme comprising: (a) incubating an enzyme-containing sample with an immobilised fluorescence-quenched peptid having the formula Que-Sub-Flu-Spa-Car or Flu-Sub-Que-Spa-Car wherein Sub is a peptide chain containing a specific cleavage site for said proteolytic enzyme; Flu is a fluorophore; Que is a quencher capable of absorbing fluorescent radiation emitted by the fluorophore; Spa is a direct bond or a spacing chain; and Car is a water-insoluble and/or macromolecular carrier; (b) optionally separating the liquid from the carrier material; (c) irradiating said carrier material and measuring fluorescence. Also disclosed are immobilised substrates containing specific amino acid sequences for use in such an assay, especially in an assay for aggrecanase, and metalloproteinase-1, -3 and -13 activity.</p>		

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Method for assaying proteolytic enzymes using fluorescence-quenched substrates

The invention relates to a method for assaying a proteolytic enzyme comprising the use of a substrate having a fluorescent label and a fluorescence quencher.

Fluorometric assays for proteolytic enzymes, wherein a peptide substrate which is specifically cleaved by the enzyme and which carries a fluorophore at one side and a fluorescence quencher at the other side of the cleavage site are used, are known in the art. For example, EP-A-428000 discloses fluorescence-quenched substrates for detection of viral proteolytic enzymes, the substrates consisting of peptide sequences that can be specifically cleaved by the viral protease, to which are attached a fluorescent donor such as 5-(2-aminoethylamino)naphthalene-1-sulphonic acid (Edans), and a quencher, such as 4-(4-dimethylaminophenylazo)benzoic acid (Dabcyl). Upon contact with the specific proteolytic enzyme, the peptide is cleaved and the fluorescent donor is detached from the quenching acceptor, so that irradiation leads to a detectable fluorescence which is a measure for the specific enzymatic activity. A similar system for the detection of retroviral proteases is disclosed in EP-A-435845. Fluorogenic substrates that can be selectively hydrolysed by matrix metalloproteinase-3 (MMP-3) and to which a substituted coumarin and 2,4-dinitrophenyl are bound as a fluorophore and a quencher respectively, are described by Nagase et al., *J. Biol. Chem.* **269**, 20952-20957 (1994). A general method for the preparation of such internally quenched fluorogenic protease substrates with the Edans/Dabcyl system, is described by Maggiora et al., *J. Med. Chem.* **35**, 3727-3730 (1992).

Although these known substrates and methods allow proteolytic enzymes to be assayed with reasonable accuracy, known substrates and methods with fluorogenic proteinase substrates have been applied with purified enzymes and hardly with complex biological media (e.g. cell culture media, synovial fluid and other tissue fluids). These substrates and methods are likely to be subject to disturbances by fluorescent or light-absorbing constituents of more complex solutions than purified enzymes. According to the invention, a method is provided for quantitatively assaying proteolytic enzymes, using immobilised fluorescence-quenched substrates.

With the immobilised fluorescence-quenched substrates, e.g. on microtiter plates, the fluorescent fragments remain attached to the insoluble carrier after proteolytic cleavage. Thus, disturbing components of the reaction mixture (e.g. blood) can easily

be washed away, providing a clean solution for use in the actual measurement. As a result, a more sensitive and reliable assessment of proteolytic enzyme activity is achieved.

Small peptide substrates for proteolytic enzymes suffer from the disadvantage that they may still be hydrolysed by high molecular weight complexes of proteinase and inhibitor, as is the case with matrix metalloproteinases inhibited by $\alpha 2$ -macroglobulin ($\alpha 2$ MG). Inasmuch as MMP- $\alpha 2$ MG complexes are unable to hydrolyse the high molecular-weight physiological substrates such as proteoglycans, plasma proteins and collagen proteins, soluble peptide substrates overestimate the actual proteolytic activity. Immobilised fluorescence-quenched proteinase substrates are not hampered by this disadvantage: as a result of their immobilisation, they are not converted any more by MMP- $\alpha 2$ MG complexes. In this event, and all events mentioned below, 'immobilised' is not limited to an insoluble carrier. Also, soluble carriers such as albumin, and macromolecules derived by any means, are applicable. In this context, macromolecules are understood as having a molecular weight of more than 5 kDa, especially more than 10 kDa.

Another aspect of the immobilisation procedure is that the carrier (microtiter plate, paper or other strip) can be dried before performing the assay. This offers the advantage that reproducible and convenient assay kits can be developed which require minimal effort of the testing person. More importantly, the "dry format assay" allows assessment of proteolytic activity without dilution of the sample: it can be applied directly to the carrier. Thus, dilution of biological samples with proteolytic enzymes containing reversible, synthetic inhibitors is avoided. This is an advantage since dilution of such samples is likely to disturb the equilibrium of proteolytic enzyme and inhibitor with the consequence that artefactual data are obtained.

Immobilisation of fluorescence-quenched substrates offers additional new possibilities to assess enzyme activity of proteinases.

1) When immobilised in acrylate gel, zymography-type of assays (see Hanemaaijer et al. *Biochem. J.* (1993) **296**, 803-809) can be performed: first the proteolytic enzymes and their pro-forms are separated on the basis of their molecular weight. After electrophoresis components like sodium dodecyl sulphate have been washed off, proteinases and proforms renature and become active. With immobilised fluorescence-quenched substrates, an increase in fluorescence is observed. Advantages over conventional

zymography are: peptides represent more general substrates (e.g. within one gel, several MMP's and proforms can be detected, in contrast to conventional zymography, where the included substrate gelatin, casein or other makes the assay more or less specific for one (group of) enzymes; selectivity towards specific proteinases can be achieved by selection of the proper peptide sequence. As such, synthetic peptides allow a far greater range of substrates to be used than physiological substrates: limited sources of, for instance collagen, are available. Furthermore, the use of immobilised fluorescence-quenched substrates allows continuous monitoring of fluorescence (in contrast to the "end point" conventional zymography method). Thus, low levels of proteinases can be detected in the presence of excessive amounts of other proteinases by determination of fluorescence at late and early points in time, respectively. Fluorescence-quenched zymography is a very sensitive technique, since fluorescence can be sensitively measured. In addition, it is a quantitative method, and it measures by an increase of a signal rather than a decrease in a signal as is the case with conventional zymography.

2) Immobilised fluorescence-quenched peptides may be applied in cell culture systems: growing cells on culture plates coated with fluorescence-quenched peptides allows assessment of production of proteolytic enzymes by the cultured cells. The peptides may also be physically (non-covalently) bound for studying cell migration.

3) Fluorescence-quenched peptides may be applied with tissue sections by bringing tissue in contact with a fluorescence-quenched substrate: fluorescence microscopy allows measurement of proteolytic enzyme activity at cellular level. This application can be performed with dissolved substrate, preferably in viscous medium such as polyvinyl alcohol or agarose to reduce diffusion of fluorescent products. Most ideally, the substrate is covalently bound to a macromolecule used to coat the histological support, or covalently bound to the support directly.

Proteinases are known to participate in tissue remodelling during physiological and pathological processes, through enzymatic digestion of various components of the extracellular matrix. Variation of active proteolytic enzymes may regulate the local accumulation or resorption of extracellular matrix, for instance in atherosclerosis, cartilage and bone turnover, and wound healing. Detection of proteolytic enzymes by immunohistology allows assessment of local amounts of proteinases. However, available antibodies do not distinguish between the pro-form, the active form, and the inhibited form of the enzyme. It would be more appropriate to have a methodology to assess the

local enzyme activity of proteolytic enzymes rather than use the known immunological detection techniques. Such activity assay has been described recently by Galis et al. (FASEB J., 9 (1995) 974-980) with in situ zymography. Like SDS-PAGE format zymography, this represents an "end point" assay. Immobilised fluorescence-quenched substrates are perfectly suitable for use in microscopic localisation of active proteinases, because such use (1) allows local measurements, (2) allows measurements in time, (3) represents a quantitative method, (4) measures increase in signal rather than decrease in signal, (5) allows tissue section to be removed with continued monitoring of fluorescence (the tissue section has made an imprint), (6) is relatively easy to perform, (7) is applicable with virtually any buffer. With respect to items 2, 4, 5, 6 and 7, immobilised fluorescence-quenched substrates are superior over in situ zymography format as described by Galis et al.

The method according to the invention comprises:

- (a) incubating an enzyme-containing sample with an immobilised fluorogenic peptide having the formula

Que-Sub-Flu-Spa-Car

or

Flu-Sub-Que-Spa-Car

wherein

Sub is a peptide chain containing a specific cleavage site for said proteolytic enzyme;

Flu is a fluorophore;

Que is a quencher capable of absorbing fluorescent radiation emitted by the fluorophore, which may also be the same groups as Flu;

Spa is a direct bond or a spacing chain; and

Car is an insoluble and/or macromolecular carrier;

(b) optionally separating the liquid from the carrier material;

(c) irradiating said carrier material and measuring fluorescence.

Apart from the symbols Flu, Sub, Que, Spa and Car defined above, the following abbreviations are used in this specification:

Aad α -aminoadipic acid

Abu α -aminobutyric acid

	Cha	β -cyclohexylalanine
	Dabcyl	4-(4-dimethylaminophenylazo)benzoic acid
	DMF	dimethylformamide
	DMSO	dimethylsulphoxide
5	DNP	dinitrophenyl
	Eaca	ϵ -aminocaproic acid
	Edans	5-(2-aminoethylamino)naphthalene-1-sulphonic acid
	EDTA	ethylenediaminetetraacetic acid
	EGS	ethyleneglycol-bis(succinimidyl succinate)
10	Emc	S-mercaptoethylcysteine
	Fmoc	9-fluorenylmethoxycarbonyl
	Gaba	γ -aminobutyric acid
	HPLC	high performance liquid chromatography
	Hse	homoserine (α -amino- γ -hydroxybutyric acid)
15	Hyp	4-hydroxyproline
	Mca	7-methoxycoumarin-4-acetic acid
	Mcc	7-methoxycoumarin-3-carboxylic acid
	MMP	matrix metalloproteinase
	Nma	N-methylantranilic acid
20	NMM	N-methylmorpholine
	NMP	N-methylpyrrolidone
	Nlc	norleucine (α -aminocaproic acid)
	Nva	norvaline (α -aminovaleric acid)
	Orn	ornithine (α,δ -diaminovaleric acid)
25	PA	plasminogen activator
	PAGE	polyacrylamide gel electrophoresis
	PBS	phosphate buffered saline
	SDS	sodium dodecyl sulphate
	Sec	S-ethylcysteine (α -amino- β -ethylthio-propionic acid)
30	Smc	S-methylcysteine (α -amino- β -methylthio-propionic acid)
	TFA	trifluoroacetic acid
	Tris	tris(hydroxymethyl)aminomethane

In the method according to the invention, the peptide chain Sub is selected in accordance with the specific proteolytic enzyme activity under assay. Proteolytic enzymes currently known can be divided in serine proteases (EC number 3.4.21), cysteine proteases (EC 3.4.22), aspartic proteases (EC 3.4.23), and metalloproteases (EC 3.4.24). For example, for the matrix metalloproteases (MMP) the cleavage site is Gly-Leu and the amino acid sequence to be recognised by the MMP enzyme may be

Pro-Xax-Gly-Leu, wherein Xax is any amino acid, in particular Pro-Gln-Gly-Leu or Pro-Leu-Gly-Leu. As another example, plasmin specifically cleaves at the carboxyl function of lysine, and the specific sequence may e.g. be Ile-Phe-Lys-Xay. These and other specific protease substrate sequences are known in the art. Clinically important
5 proteases comprise the following: factor VIIa, factor IXa, factor Xa, APC, thrombin, t-PA, u-PA, plasmin, trypsin, chymotrypsin, enterokinase, pepsin, cathepsins, angiotensin converting enzyme, matrix metalloproteinases (collagenases, stromelysins, gelatinases), elastase, Cir and Cis.

Some proteases with the relevant substrate specificity are as follows:

10 Cathepsin C: Cysteine protease catalysing the successive removal of N-terminal dipeptides from polypeptides. The reaction rate is dependent on the penultimate amino acid, whereby hydrophilic and hydrophobic residues are accepted. Degradation is blocked by N-terminal Lys or Arg. Pro as the second or third amino acid also prevents cleavage.

15 Chymotrypsin: Serine endopeptidase specifically hydrolysing peptide bonds at the C-termini of Tyr, Phe and Trp. Leu, Ala, Asp and Glu are cleaved at lower rates. Acts also upon amides and esters of susceptible amino acids.

Elastase: Serine endopeptidase, hydrolysing peptide bonds at the C-terminal side of amino acids with uncharged non-aromatic side chains like Ala, Val, Leu, Gly and Ser.

20 Factor Xa: Serine endopeptidase, hydrolysing specifically peptide bonds at the carboxylic side of Arg within the sequence -Ile-Glu-Gly-Arg-Xaz (Xaz is any amino acid).

Kallikrein: Serine endopeptidase, preferentially hydrolysing peptide and ester bonds at the carboxylic side of Arg, especially at Phe-(or Leu)-Arg-Xaz bonds.

25 Pepsin: Aspartic endopeptidase with broad specificity. Cleaves preferentially bonds at the carboxylic side of Phe, Met, Leu or Trp which is bound to another hydrophobic residue. Tyr-Xaz bonds are relatively resistant.

Plasmin: Serine endopeptidase hydrolysing peptide and ester bonds at the carboxylic side of Lys or Arg.

30 Subtilisin: Unspecific serine endopeptidase that cleaves most peptide bonds, especially those adjacent to Asp, Glu, Ala, Gly and Val.

Thermolysin: Unspecific Zn-metalloproteinase that hydrolyses peptide bonds involving the amino group of hydrophobic amino acids with bulky side chains like Ile, Leu, Met,

Phe, Trp and Val. The presence of Pro at the C-terminus of a hydrophobic amino acid prevents cleavage at the N-terminus of the latter.

Thrombin: Serine endopeptidase, hydrolysing specifically proteins and peptides at the carboxylic side of the basic amino acids Arg and Lys. Amide and ester bonds of Arg and Lys are cleaved as well.

Trypsin: Serine endopeptidase, hydrolysing specifically proteins and peptides at the carboxylic side of the basic amino acids Arg and Lys. Amide and ester bonds of Arg and Lys are also cleaved.

The method is suitable e.g. for assaying aggrecanase activity. Known aggrecanase cleavage sites (shown below with Δ) that can be used in such an assay include the following:

369	Ile-Thr-Glu-Gly-Glu Δ Ala-Arg-Gly-Ser- ³⁷⁸ Val	human and bovine aggrecan
369	Ile-Thr-Glu-Gly-Glu Δ Ala-Arg-Gly-Asn- ³⁷⁸ Val	rat aggrecan
1541	Ala-Ser-Glu-Leu-Glu Δ Gly-Arg-Gly-Thr- ¹⁵⁵⁰ Ile	human aggrecan; similar
15	sequence in rat aggrecan (residues 1270-1279)	
1710	Phe-Lys-Glu-Glu-Glu Δ Gly-Leu-Gly- ¹⁷¹⁸ Ser	human aggrecan; similar
	sequence in bovine aggrecan (residues 1459-1467)	
1455	Phe-Arg-Glu-Glu-Glu Δ Gly-Leu-Gly- ¹⁷¹⁸ Ser	rat aggrecan
1815	Pro-Thr-Ala-Gln-Glu Δ Ala-Gly-Glu-Gly- ¹⁸²⁴ Pro	human aggrecan; similar
20	sequence in bovine aggrecan (residues 1564-1573) and rat aggrecan (residues 1560-1569)	
1915	Thr-Ile-Ser-Gln-Glu Δ Leu-Gly-Gln-Arg- ¹⁹²⁴ Pro	human aggrecan
1664	Thr-Val-Ser-Gln-Glu Δ Leu-Gly-Gln-Arg- ¹⁶⁷³ Pro	bovine aggrecan
1660	Thr-Val-Ser-Gln-Glu Δ Leu-Gly-His-Gly- ¹⁶⁶⁹ Pro	rat aggrecan

25 These sequences have SEQ ID No's: 1-9, respectively.

In these sequences, the underlined part should be present, optionally with conserved mutations, e.g. Ala, Abu, Val, Nva or Leu for Gly; Ala, Abu, Val, Nva, Ile or Nle for Leu; Gly, Abu, Val, Nva, Leu, Ile or Nle for Ala; Gln/Glu, Asn/Asp or Aad for Glu or Gln; Lys, Orn, His or Trp for Arg. Preferably one more amino acid at either side, particularly two more and optionally three more amino acids at either side of the underlined part are present, also possibly with conserved mutations. It is often advantageous to include in the substrate a further partial sequence of e.g. 50-150 amino acids corresponding to the relevant aggrecan either in the sequence Sub or in Car or in

Spa. For the aggrecans, such a further sequence is preferably derived from the C-terminal region with respect to the cleavage site. An example is the human aggrecan sequence 382-477 as depicted in SEQ ID No: 10, which may contain one or more mutations.

5 The method is also suitable e.g. for assaying degradation of aggrecan by matrix metalloproteinases. The known MMP cleavage site (shown below with Δ) that can be used in such an assay includes the sequence:
³³⁴Asp-Phe-Val-Asp-Ile-Pro-Asn Δ Phe-Phe-Gly-Val-Gly-Gly-³⁴⁸Glu (SEQ ID No: 11) (human aggrecan, cleavage by MMP-1, -2, -3, -7, -8, -9, and -13). In the
 10 sequence of the substrate, the underlined part should be present, conservative exchanges of ³³⁹Pro (e.g. by Hyp) and ³⁴²Phe (e.g. by Tyr, Trp or Cha) being allowed. Preferably, one more amino acid at either side, particularly two more and optionally three more amino acids at either of the underlined part is present. Here also, it may be advantageous to include a further partial sequence of e.g. 50-150 amino acids corresponding to the
 15 relevant aggrecan, which may be derived both from the N-terminal side and from the C-terminal side of the cleavage site.

 The method is also suitable e.g. for assaying matrix metalloproteinase activity. Cleavage sites that can be used specifically e.g. for an MMP-13 assay include the
 20 sequence Ala-Arg-Gly-Ser, wherein Ala and Gly may be replaced by another aliphatic amino acid and Ser may be replaced by another hydroxy-aliphatic or aliphatic amino acid. Thus, a selective substrate for MMP-13 may be e.g. Dabcyl-Gaba-Ile-Thr-Glu-Gly-Gly-Ala-Arg Δ Gly-Ser-Glu(Edans)-Ile-Lys-NH₂) (SEQ ID No: 12). Another cleavage site that can be used specifically for an MMP-13 assay includes the sequence
 25 Arg-Gly-Leu-Glu, wherein Arg may be replaced by another positively charged amino acid, or analogue, and Gly and/or Leu may be replaced by another aliphatic amino acid. Thus, a selective substrate for MMP-13 may be e.g. Dabcyl-Gaba-Pro-Arg-Gly Δ Leu-Glu(Edans)-Ala-Lys-NH₂.

 Similarly, Dabcyl-Gaba-Arg-Pro-Lys-Pro-Val-Glu Δ Nva-Trp-Arg-Glu-(Edans)-Gly-Lys-NH₂ (SEQ ID No: 13) may be used as a selective fluorescence-
 30 quenched substrate for stromelysin (MMP-3); the amino acid sequence thereof was found by of Nagase et al (Nagase H, Fields CG, Fields GB. J. Biol. Chem. 269 (1994) 20952-20957) to be highly selective for MMP-3. The subsequence (Pro)-Val-Glu-Nva-Trp-(Arg) should be present, with possible conserved variations.

Also Dabcyl-Gaba-Pro-Cha-Abu-Smc-His-Ala-Glu(Edans)-Gly-Lys-NH₂ (SEQ ID No: 14) may be used as a selective substrate for assaying enzyme activity of interstitial collagenase (MMP-1); the amino acid sequence Cha-Abu-Smc-His was found by McGeehan et al. (McGeehan GM, Bickett DM, Green M, Kassel D, Wiseman JS, Berman J., J. Biol. Chem. 269 (1994) 32814-32820) to form a superior substrate over the natural sequence Leu-Gly-Leu-Trp. Variations thereof, such as Leu for Cha; Gly or Ala for Abu; Leu, Sec or Emc for Smc; and Trp for His, are also useful.

The fluorophore (Flu) can be a substituted amino acid or another substituted group capable of being attached to a peptide sequence, such as a substituted mercapto-acid, wherein the side-chain of the amino acid or other group carries the fluorescent moiety. The substituted amino acid may be a lysine, ornithine or other α,ω -diamino acid, to which the fluorescent moiety is bonded at an amino group, or Glu, Asp or Aad, to which the fluorescent moiety is bound by means of the terminal carboxyl function, or cysteine or other thiol-containing amino acid binding the fluorescent moiety through the thiol function.

Instead of being attached at the side chain of the peptide chain, the fluorophore may be attached between two amino acids, and thus be positioned in the peptide chain. In this embodiment, the fluorophore may contain e.g. an amino, mercapto, or hydroxy function at one end, and a carboxy function at the other end.

Fluorophores to be used in the substrates are known in the art. Suitable fluorophores comprise Edans described above and other aminonaphthalenesulphonic acids, coumarin, substituted coumarins such as 7-methoxycoumarin-4-acetic acid (Mca) or 7-methoxycoumarin-3-carboxylic acid (Mcc), tryptophane, N-methylantranilic acid (Nma). The fluorophores may have excitation wavelengths between e.g. 250 and 400 nm and emission wavelengths e.g. between 370 and 550 nm.

The quencher (Que) can be attached to the specific substrate sequence e.g. by means of its carboxyl function, optionally through one or more spacing amino acids such as ω -amino-alkanoic acids, in particular γ -aminobutyric acid (Gaba), ϵ -aminocaproic acid (Eaca), ornithine or lysine. If the quencher is placed between the fluorophore and the carrier (formula Flu-Sub-Que-Spa-Car), it may be attached at the side chain of an amino acid or in between two amino acids, as described above for Flu.

Quenchers to be used in the substrates are known in the art. Suitable quenchers include Dabcyl described above and other aminophenylazobenzoyl derivatives and di-

nitrophenyl (DNP) and derivatives. The quencher preferably has an absorption wavelength that corresponds to the emission wavelength of the fluorophore. Therefore the quencher and the fluorophore are matched. Examples of suitable combinations of fluorophore and quencher are Edans/Dabcyl, coumarin/DNP, tryptophane/DNP and Nma/DNP. Since quenching of fluorescence may also occur between two identical fluorophores, efficient quenching can also be achieved when $Q_{uc} = F_{lu}$. The fluorophore and the quencher should be placed at such a distance that intramolecular energy transfer between the two is possible. This requirement will usually be met when the amino acid chain between the fluorophore and the quencher comprises 4–10 amino acids, especially 5–8 amino acids, or when the spatial distance between the fluorophore and the quencher corresponds to such a chain distance.

The spacing chain Sp_a may be a direct bond, a chain of one or more atoms, or a peptide or other chain providing sufficient distance between the substrate peptide and the insoluble carrier. The spacing chain can e.g. comprise one or more ω -amino acids such as Eaca. At its terminus, the spacing chain contains a group capable of covalent or other (e.g. biotin/avidin) coupling to the insoluble carrier. Coupling with the carrier may be established through homo- or bifunctional crosslinking agents coupling with amino, thiol or carboxyl functions. Suitable crosslinking or coupling agents include glutaric dialdehyde and commercially available amino-, sulfo- or carbo-link reagents. Coupling can also be performed by acrylate derivatives which can be incorporated in a polyacrylate matrix.

Preferably, the spacing chain and the carrier are bound to the substrate chain at its carboxyl terminus. If it is necessary for the coupling group at the end of the spacing chain to be bound to an amino terminus of the spacing chain, the "polarity" of the amino acid chain can be inversed by the introduction of e.g. a lysine or other α,ω -diamino acid. For example, a suitable spacing chain consists of a lysine residue, to which at its ω -amino position a Eaca residue is bound, to which, in turn, an acryloyl group is bound.

The insoluble and/or macromolecular carrier Car can comprise any conventional solid support used in biochemical assays. These include microtiter plates, paper strips, synthetic polymer strips, beads, resins, acrylate matrices (e.g. gels), glass, for instance after coating, and proteins.

The insoluble and/or macromolecular carrier Car can also comprise a macro-

molecular, dispersed or soluble, structure for use of the substrate as a model for natural enzyme substrates. This is especially useful when measuring enzyme activity depending on inhibitors and the like: a relatively small synthetic substrate not having a macromolecular carrier could be cleaved despite the presence of an inhibiting complex and thus measure an activity that would not be available for a "natural" macromolecular substrate.

The sequence Que-Sub-Flu-Spa-Car described above is often preferred over the sequence Flu-Sub-Que-Spa-Car, except when used as a macromolecular, dispersed or soluble substrate as describe above.

In a typical arrangement, a plurality of groups Flu-Sub-Que-Spa- is attached to a single carrier, resulting in the formula $(\text{Flu-Sub-Que-Spa})_n\text{-Car}$. In exceptional cases where a high density of fluorophores is present (e.g. when $n \geq 20$, e.g. between 50 and 100), efficient quenching may be achieved without Que groups.

The method of the invention allows enzyme assays in various embodiments:
1) determination of enzyme activities in zymography format (substrate immobilised in/on acrylate gel); 2) enzyme measurement in microtiter plates and on or in other solid supports, allowing undiluted biological samples to be assayed and disturbing constituents of the biological matrix to be easily washed out; 3) assessment of proteolytic enzyme activity in tissue sections (histology); 4) enzyme measurement in solution or dispersion to mimic natural macromolecular substrates.

The proteolytic enzymes to be assayed using the method of the invention comprise all proteases including serine proteinases, cysteine proteinases, aspartic proteinases and metalloproteinases. The method is particularly useful with endoproteinases. A preferred class of proteinases to be assayed with the present method comprises the matrix metalloproteinases (MMP's) including collagenases, gelatinases and stromelysins. The MMP's play a role in wound healing, rheumatoid arthritis and osteoarthritis, tumor invasion and angiogenesis, through cell migration, cartilage degradation and basal membrane degradation and metastasis, respectively, and thus the activity of these enzymes is an important indicator for these conditions. An important advantage of the present method is that not only the active enzymes (MMP's) are detectable, but also the pro-enzymes, if the substrate is immobilised on or in acrylamide gel in zymography format.

The method of the invention can further be improved by selective removal,

prior to the assay of the proteinase under investigation, of other proteolytic enzymes, e.g. using specific antibodies or other selective binding agents, by selective binding of the proteinase under investigation (with antibodies or other selective binding techniques) followed by separation of the unbound enzymes, or by addition of selective inhibitors of other proteolytic enzymes, or by addition of a selective inhibitor of the proteinase under investigation; in this latter case, the final result is obtained by subtraction of the activity measured after inhibition from the total activity measured. All such assays include measurements of enzyme activities without sample pretreatment, or with any form of pretreatment of the biological sample including activation of pro-enzymes.

10 EXAMPLES

EXAMPLE 1:

Synthesis of fluorogenic peptides

Synthesis of Fmoc-Glu(Edans)-OH

To a stirred solution of Fmoc-Glu(OH)-O-tert-butyl (1.7 g, 4 mmol), Edans (1.07 g, 4 mmol) and benzotriazole-1-yloxy-tris(dimethylamino)-phosphonium hexafluorophosphate (1.77 g, 4 mmol) in 10 ml DMF was added at room temperature to di-isopropylethylamine (2ml, 12 mmol, distilled from CaH_2). After 2 h the reaction was complete (silica thin layer chromatography with toluene/acetic acid, 9/1, v/v). To the reaction mixture was added 50 ml CH_2Cl_2 and 50 ml 0.5 M KHSO_4 . The organic layer was washed with 0.1 M KHSO_4 and H_2O , dried on MgSO_4 , and evaporated *in vacuo* to yield 2.8 g of oil. To remove the tert-butyl group, 10 ml glacial acetic acid and 1 ml 12 N HCl were added. After stirring for 1 h, the solvents were evaporated *in vacuo*. Traces of acetic acid were removed by co-evaporation with DMF (2 x 10 ml). The product was purified by reverse-phase HPLC (RP-HPLC) in 45 % yield (C18 column using a acetonitrile gradient in 0.1 % TFA in H_2O).

Synthesis of fluorescence-quenched Dabcyl/Edans peptides

Substrates were synthesised at 10 μmol scale by solid phase chemistry on an automated multiple synthesiser using tentagelS AC (loading 0.2 μeq , particle size 90 μm). Repetitive couplings were performed by adding a mixture of 90 μl 0.67 M PyBOP (benzotriazole-1-yl-oxy-tris-pyrrolidino-phosphonium hexafluorophosphate) in NMP, 20 μl NMM (N-methylmorpholine) in NMP (2/1, v/v) and 100 μl of an 0.6 M solution of the appropriate Fmoc-amino acid in NMP. Coupling of Fmoc-Glu(Edans)-OH was

performed with a 10-fold excess for 3 h. The DabcyI moiety was coupled with a suspension of 10 equivalents p-(p-dimethylamino-phenylazo)benzoic acid, 10 equivalents PyBOP and 20 equivalents NMM in 250 μ l NMP for 3 h. Cleavage from the resin and removal of the protecting groups was performed by adding 200 μ l TFA/H₂O (19/1, v/v) to the reaction vessel (6 times at 5 min intervals). Three hours after the first
5 TFA/H₂O addition, the peptides were precipitated from the combined filtrates by addition of 10 ml ether/pentane (1/1, v/v) and cooling to -20°C, after which the peptides were isolated by centrifugation (-20°C, 2,500 g, 10 min.). Subsequently, peptides were purified by RP-HPLC with a SuperPac Pep-S 15 μ m 9.3 x 250 mm column. Purity and identity of the peptides was established by RP-HPLC (acetonitrile gradient in 0.1 %
10 TFA in H₂O) and by TOF-MALDI mass spectrometry.

Thus, fluorescence-quenched DabcyI-Gaba-Ile-Thr-Glu-Gly-Glu Δ Ala-Arg-Gly-Ser-Glu(Edans)-Ile-Lys-NH₂ (SEQ ID No: 15) was synthesised as a fluorescence-quenched substrate for aggrecanase, to be coupled to a carrier protein of about 100
15 amino acids, and DabcyI-Gaba-Pro-Gln-Gly Δ R as substrates for MMPs (examples of R: -Leu-Phe-Ala-Glu(Edans)-Ala-Lys-NH₂ (SEQ ID No: 16); -Leu-Phe-Gly-Glu(Edans)-Lys-NH₂ (SEQ ID No: 17); -Leu-Glu(Edans)-Ala-Lys-NH₂ (SEQ ID No: 18); -Leu-Glu(Edans)-Gly-Lys-NH₂ (SEQ ID No: 19); -Leu-Glu(Edans)-Gly-NH₂ (SEQ ID No: 19 without terminal Lys); Δ , cleavage site). Moreover, R = Ala-Arg Δ -
20 Gly-Ser-Glu(Edans)-Ile-Lys-NH₂ (SEQ ID No: 20) was prepared as a selective substrate for MMP-13. In addition, DabcyI-Gaba-Pro-Arg-Gly Δ Leu-Glu(Edans)-Ala-Lys-NH₂ (SEQ ID No: 21) was synthesised as a selective substrate for MMP-13. In this latter sequence Leu may be replaced or even deleted.

EXAMPLE 2:

25 *Immobilisation of fluorescence-quenched peptides on silica beads*

To 1.0 ml of fluorescence-quenched peptide solution (DabcyI-Gaba-Pro-Gln-Gly Δ R; 25 μ M in phosphate buffered saline, R contains a lysine residue used for the immobilisation), 10 mg of aminopropyl silica beads (40 μ m diameter, 1.4 mmol amino groups per gram) was added. After 15 minutes of mixing at room temperature, 20 μ l EGS solution
30 (25 mM in DMSO) was added. The decline in A₄₇₀ (absorbance maximum of DabcyI) of the supernatant was used to monitor the reaction. Coupling was continued until A₄₇₀ ceased to decrease. After centrifugation and removal of the supernatant, beads were

washed successively with PBS (1.5 ml), PBS with 0.1% Tween-20 (1.5 ml), 1 M Tris HCl (pH 7.5; 1.2 ml), and incubation buffer (50 mM Tris, pH 7.6; 150 mM NaCl, 5 mM CaCl_2 , 1 μM ZnCl_2 , 0.01% Brij-35; 1.0 ml).

5 Upon incubation of peptide-labelled silica beads with a mixture of activated gelatinases (MMP-2 and MMP-9), the Dabcyl-Gaba-Pro-Gln-Gly fragment was effectively released from the beads into the supernatant, as verified by RP-HPLC (C18 column using a acetonitrile gradient in 0.1 % TFA in H_2O).

EXAMPLE 3:

Immobilisation of fluorescence-quenched peptides on glass slides

10 Glass microscope slides were thoroughly cleaned by washing in 20% H_2SO_4 , water (two times), 0.1 N NaOH, and water. After drying, the glass slides were placed in 3-aminopropyltriethoxysilane for 4 minutes at room temperature, and rinsed with water and PBS (2 times). Under gentle agitation, glass slides were immersed in a solution of fluorescence-quenched substrate (e.g. Dabcyl-Gaba-Pro-Gln-Gly- Δ Leu-Phe-Ala-Glu(Edans)-Ala-Lys- NH_2 (SEQ ID No: 16) or Dabcyl-Gaba-Pro-Gln-Gly- Δ Leu-Glu(Edans)-Ala-Lys- NH_2 (SEQ ID No: 18); 25 μM in 1.0 ml PBS), to which 20 μl EGS (25 mM in DMSO) was added subsequently. Monitoring of A470 showed that coupling was complete within three hours at room temperature. Blocking of N-hydroxy-succinimidyl groups resulting from excess EGS was performed by addition of glycine
15 in PBS (50 mM final concentration, 1.0 ml) for 1 hr. All steps were performed at ambient temperature.

Glass slides coated with fluorescence-quenched substrates were used to detect MMP activity in tissue sections as follows: cryostat sections (5 μm) of rabbit calvarial periost were placed on a substrate coated glass slide and incubated at 37°C in a humid
25 atmosphere in incubation buffer (50 mM Tris, pH 7.6, 5 mM CaCl_2 , 1 μM ZnCl_2 , 1 mM 4-aminophenylmercuric acetate). Appearance of fluorescence was followed with a fluorescence microscope. With time, increase in fluorescence was observed at the site of the tissue, as distinct fluorescent spots (Fig. 1). No fluorescence was detectable at sites of the glass not covered with tissue. Tissue sections incubated in the presence of
30 EDTA or a synthetic MMP inhibitor showed substantially lower fluorescence. Furthermore, fluorescence of tissue sections not activated with 4-aminophenylmercuric acetate was lower than that of sections activated with 4-aminophenylmercuric acetate.

EXAMPLE 4:

Fluorescence-quenched peptides coupled to bovine serum albumin

Fluorescence-quenched substrate (e.g. Dabcyl-Gaba-Pro-Gln-Gly- Δ Leu-Phe-Ala-Glu-(Edans)-Ala-Lys-NH₂ (SEQ ID No: 16); final concentration, 25 μ M in PBS) was conjugated to bovine serum albumin (BSA; 2 mg/ml final concentration in PBS) by EGS (final concentration 0.5 mM; final volume, 2 ml) as described above. RP-HPLC analysis (linear gradient of acetonitrile in 0.1 % TFA/H₂O) of incubations of the BSA-substrate with MMP-9 confirmed proteolysis of the protein-coupled substrate: after precipitation of protein, the Dabcyl-Gaba-Pro-Gln-Gly fragment was detected in the supernatant.

10 EXAMPLE 5:

Fluorescence-quenched MMP substrate that is not converted by α 2-macroglobulin-complexed MMP

Fluorescence-quenched substrate (e.g. Dabcyl-Gaba-Pro-Gln-Gly- Δ Leu-Phe-Ala-Glu-(Edans)-Ala-Lys-NH₂ (SEQ ID No. 16); 1 mM DMSO, 200 μ l) was derivatised with N-succinimidyl-S-acetylthioacetate (10 mM in DMSO, 50 μ l), in the presence of triethylamine (100 mM in DMSO, 10 μ l) for 30 minutes at room temperature. After de-acetylation of 80 nmol of the derivatised substrate (dissolved in 20 μ l water; reacted with 25 μ l sodium phosphate buffer, 50 mM, pH 7.5, comprising 25 mM EDTA and 0.5 M hydroxylamine, for 15 minutes at room temperature), 10 μ l of maleimide activated ovalbumin (10 mg/ml; Pierce) was added. After 2 hours at room temperature, excess maleimide-ovalbumin was inactivated by addition of L-cystein (10 μ l 20 mM in water). After dialysis (10 kDa cut off membrane) against water and incubation buffer (50 mM Tris, pH 7.6, 150 mM, NaCl, 5 mM CaCl₂, 1 μ M ZnCl₂, 0.01% Brij-35), conversion of the ovalbumin-coupled substrate by MMP-13 (0.5 nM) was determined by the rate of increase of fluorescence (excitation, 360 nm; emission, 490 nm; fluorescence units per time).

In the presence of excess α 2-macroglobulin (5 nM; pre-incubated with MMP-13 for 2 hours at 25°C), less than 5% of the ovalbumin-coupled substrate was degraded compared to incubations lacking α 2-macroglobulin. This indicates that assays with fluorescence-quenched substrates bound to a carrier do reflect inhibition of MMP activity by complexing with α 2-macroglobulin.

EXAMPLE 6:*Incorporation of fluorescence-quenched peptides into polyacrylamide*

Fluorescence-quenched substrate (e.g. Dabcyl-Gaba-Pro-Gln-Gly- Δ Leu-Phe-Ala-Glu-(Edans)-Ala-Lys-NH₂ (SEQ ID No: 16) and Dabcyl-Gaba-Pro-Gln-Gly- Δ Leu-Glu-(Edans)-Ala-Lys-NH₂ (SEQ ID No: 18); 25 nmol in 100 μ l anhydrous DMSO) is
5 derivatised into its acrylate derivative by addition of 75 nmol of N-(6-succinimidyl-oxy-6-oxyhexyl)-acrylamide or N-(4-succinimidyl-oxy-4-oxybutyl)-6-acrylamido-hexanamide dissolved in anhydrous DMSO (5 mM), and 75 nmol of triethylamine (25 mM in anhydrous DMSO). The reaction was performed at room temperature and
10 was complete after 3 hours (RP-HPLC).

Acrylate derivatives of fluorescence-quenched peptides were purified by RP-HPLC (acetonitrile gradient in 0.1 % TFA/H₂O). After lyophilisation, 12.5 nmol of acrylate derivative was mixed with 3 ml (for 1 gel) of 10% acrylamide/bisacrylamide solution (75/2, v/v), followed by casting an SDS-PAGE gel according to standard procedures.
15 Samples with matrix metalloproteinases or mixtures thereof, including inactive pro-forms were applied (20 μ l) followed by conventional SDS-PAGE electrophoresis (8 mA per gel, 4°C, 4 hours). After electrophoresis, acrylamide gels were washed 3 times for 30 minutes in wash buffer (50 mM Tris, pH 7.6, 5 mM CaCl₂, 1 μ M ZnCl₂, 2.5 % Triton X-100) and two times for 10 minutes in incubation buffer (50 mM Tris, pH 7.6;
20 150 mM NaCl, 5 mM CaCl₂, 1 μ M ZnCl₂, 0.01% Brij-35). After overnight incubation of the gel at 37°C in incubation buffer, the gel was placed under UV-light (366 nm) and fluorescent bands at molecular weights corresponding to the matrix metalloproteinases and their pro-forms were observed (Fig. 2).

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Nederlandse Organisatie voor TNO
- (B) STREET: Schoemakerstraat 97
- (C) CITY: Delft
- (E) COUNTRY: NL
- (F) POSTAL CODE (ZIP): 2628 VK

(ii) TITLE OF INVENTION: Method for assaying proteolytic enzymes using
fluorescence-quenched substrates

(iii) NUMBER OF SEQUENCES: 1

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/NL97/000..

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Ile	Thr	Glu	Gly	Glu	Ala	Arg	Gly	Ser	Val
1				5					10

(3) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Ile	Thr	Glu	Gly	Glu	Ala	Arg	Gly	Asn	Val
1				5					10

(4) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Ala	Ser	Glu	Leu	Glu	Gly	Arg	Gly	Thr	Ile
1				5					10

(5) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Phe	Lys	Glu	Glu	Glu	Gly	Leu	Gly	Ser
1				5				

(6) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Phe	Arg	Glu	Glu	Glu	Gly	Leu	Gly	Ser
1				5				

(7) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Pro Thr Ala Gln Glu Ala Gly Glu Gly Pro
1 5 10

(8) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Thr Ile Ser Gln Glu Leu Gly Gln Arg Pro
1 5 10

(9) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Thr Val Ser Gln Glu Leu Gly Gln Arg Pro
1 5 10

(10) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Thr Val Ser Gln Glu Leu Gly His Gly Pro
1 5 10

(11) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```

Val Lys Pro Ile Phe Glu Val Ser Pro Ser Pro Leu Glu Pro Glu Glu
1           5           10           15
Pro Phe Thr Phe Ala Pro Glu Ile Gly Ala Thr Ala Phe Ala Glu Val
          20           25           30
Glu Asn Glu Thr Gly Glu Ala Thr Arg Pro Trp Gly Phe Pro Thr Pro
          35           40           45
Gly Leu Gly Pro Ala Thr Ala Phe Thr Ser Glu Asp Leu Val Val Gln
          50           55           60
Val Thr Ala Val Pro Gly Gln Pro His Leu Pro Gly Gly Val Val Phe
65           70           75           80
His Tyr Arg Pro Gly Pro Thr Arg Tyr Ser Leu Thr Phe Glu Glu Ala
          85           90           95

```

(12) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```

Asp Phe Val Asp Ile Pro Asn Phe Phe Gly Val Gly Gly Glu
1           5           10

```

(13) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Ile	Thr	Glu	Gly	Gly	Ala	Arg	Gly	Ser	Glu	Ile	Lys
1				5					10		

(14) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURES:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note = Val is norvaline

(ix) FEATURES:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /note = Glu is substituted with Edans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Arg	Pro	Lys	Pro	Val	Glu	Val	Trp	Arg	Glu	Gly	Lys
1				5					10		

(15) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURES:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note = Ala is cyclohexylalanine

(ix) FEATURES:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note = Ala is alpha-aminobutyric acid

(ix) FEATURES:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note = Met is S-methylcysteine

(ix) FEATURES:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note = Glu is substituted with Edans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Pro Ala Ala Met His Ala Glu Gly Lys
1 5

(16) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURES:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /note = Glu is substituted with Edans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Ile Thr Glu Gly Glu Ala Arg Gly Ser Glu Ile Lys
1 5 10

(17) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURES:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note = Glu is substituted with Edans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Pro Gln Gly Leu Phe Ala Glu Ala Lys
1 5

(18) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURES:
 - (A) NAME/KEY: misc-feature
 - (B) LOCATION: 7
 - (D) OTHER INFORMATION: /note = Glu is substituted with Edans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Pro Gln Gly Leu Phe Gly Glu Lys
1 5

(19) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURES:
 - (A) NAME/KEY: misc-feature
 - (B) LOCATION: 5
 - (D) OTHER INFORMATION: /note = Glu is substituted with Edans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Pro Gln Gly Leu Glu Ala Lys
1 5

(20) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURES:
 - (A) NAME/KEY: misc-feature
 - (B) LOCATION: 5
 - (D) OTHER INFORMATION: /note = Glu is substituted with Edans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Pro Gln Gly Leu Glu Gly Lys
1 5

(21) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURES:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /note = Glu is substituted with Edans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Pro Gln Gly Ala Arg Gly Ser Glu Ile Lys
1 5 10

(22) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURES:

- (A) NAME/KEY: misc-feature
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note = Glu is substituted with Edans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Pro Arg Gly Leu Glu Ala Lys
1 5

Claims

1. Method for assaying a proteolytic enzyme comprising:

- (a) incubating an enzyme-containing sample with an immobilised fluorescence-quenched peptide having the formula

Que-Sub-Flu-Spa-Car

or

Flu-Sub-Que-Spa-Car

wherein

Sub is a peptide chain containing a specific cleavage site for said proteolytic enzyme;

Flu is a fluorophore;

Que is a quencher capable of absorbing fluorescent radiation emitted by the fluorophore;

Spa is a direct bond or a spacing chain; and

Car is an water-insoluble and/or macromolecular carrier;

- (b) optionally separating the liquid from the carrier material;

- (c) irradiating said carrier material and measuring fluorescence.

2. Method according to claim 1, wherein Flu is an aminonaphthalenesulphonic acid group such as Edans, and Que is an aminophenylazobenzoyl group such as Dabcyl.

3. Method according to claim 1 or 2, wherein Car is a polyacrylate or polyacrylamide.

4. Method according to any one of claims 1-3, wherein Sub contains the amino acid sequence Xab-Glu-Xad-Xac, wherein Xab is any amino acid, preferably Gly, Ala, Abu, Val, Nva, Leu, Glu or Gln, Xad is any amino acid, preferably Gly, Ala, Abu, Val, Nva or Leu, and Xac is any amino acid, preferably Arg, Gly, Ala, Abu, Val, Nva or Leu, especially Arg or Gly, for assaying aggrecanase activity.

5. Method according to any one of claims 1-3, wherein Sub contains the amino acid sequence Xai-Asn-Phe-Xaj, wherein Xai is any amino acid, preferably Pro or Hyp, and Xaj is any amino acid, preferably Phe, Tyr, Trp or Cha, for assaying aggrecan degradation by matrix metalloproteinases.

5 6. Method according to any one of claims 1-3, wherein Sub contains the amino acid sequence Xad-Arg-Xaf-Xag, wherein Xad is any amino acid, preferably Gly, Ala, Abu or Val, Xaf is any amino acid, preferably Gly or Ala, and Xag is any amino acid, preferably Ser, Thr, Ala, Abu or Hse, or the amino acid sequence Xam-Xan-Xao-Glu, wherein Xam is any amino acid, preferably Arg, Lys, Orn, His or Trp, especially Arg, 10 Xan is any amino acid, preferably Gly, Ala, Abu or Val, especially Gly, Xao is any amino acid, preferably Ala, Abu, Val, Nva, Leu, Nle or Ile, especially Leu, for assaying matrix metalloproteinase-13 activity.

7. Method according to any one of the preceding claims wherein said immobilised peptide is covalently or non-covalently bound to a solid support, such as a glass plate, 15 for assaying proteinase activity in tissue sections.

8. Immobilised substrate for assaying a proteolytic enzyme, containing a fluorescence-quenched peptide having the formula

Que-Sub-Flu-Spa-Car

or

20 Flu-Sub-Que-Spa-Car

wherein

Sub is a peptide chain containing a specific cleavage site for said proteolytic enzyme;

Flu is a fluorophore;

25 Que is a quencher capable of absorbing fluorescent radiation emitted by the fluorophore;

Spa is a direct bond or a spacing chain; and

Car is an insoluble and/or macromolecular carrier selected from a glass or polymer bead, a glass plate, a microtiter plate, a paper or synthetic polymer strip, or an acrylate or acrylamide gel. 30

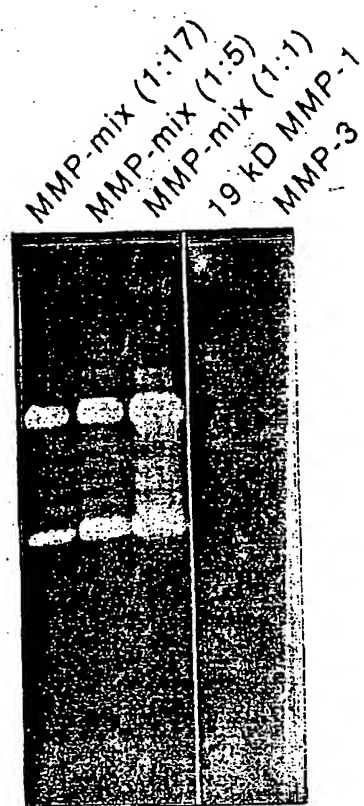
9. Labelled oligopeptide as a substrate for aggreganase activity comprising the amino acid sequence Xab-Glu-Xad-Xae, wherein Xab is any amino acid, preferably Gly, Ala, Abu, Val, Nva, Leu, Glu or Gln, especially Gly, Gln or Glu, Xad is any amino acid, preferably Gly, Ala, Abu, Val, Nva or Leu, especially Gly or Ala, and Xae is any amino acid, preferably Arg, Gly, Ala, Abu, Val, Nva or Leu, especially Arg or Gly.
10. Oligopeptide according to claim 9, comprising the amino acid sequence Xaa-Xab-Glu-Xad-Xae-Xaf, wherein Xaa is Glu, Gln, Ala, Ser or Thr, and/or Xaf is Gly, Glu or Gln, and Xab, Xad and Xae are as defined in claim 8.
11. Oligopeptide according to claim 9, comprising one of the following sequences:
Gly-Glu-Ala-Arg, Leu-Glu-Gly-Arg, Glu-Glu-Gly-Leu, Gln-Glu-Ala-Gly and Gln-Glu-Leu-Gly, in particular the sequence Gly-Glu-Ala-Arg.
12. Labelled oligopeptide as a substrate for aggregan degrading activity by matrix metalloproteinases comprising the amino acid sequence Xah-Xai-Asn-Phe-Xaj-Xak, wherein Xah is any amino acid, especially Ala, Abu, Val, Nva, Leu, Nle or, most especially, Ile, Xai is any amino acid, preferably Pro or Hyp, and Xaj is any amino acid, preferably Phe, Tyr, Trp or Cha, and Xak is any amino acid, especially Ala, Abu, Val, Nva, Ile, Leu or, most especially, Gly.
13. Labelled oligopeptide as a substrate for matrix metalloproteinase-13 activity, comprising the amino acid sequence Xad-Arg-Xaf-Xag, wherein Xad is any amino acid, preferably Gly, Ala, Abu or Val, Xaf is any amino acid, preferably Gly or Ala, and Xag is any amino acid, preferably Ser, Thr, Ala, Abu or Hsc, in particular the sequence Ala-Arg-Gly-Ser.
14. Oligopeptide according to claim 13 as a specific substrate for matrix metalloproteinase-13 activity, comprising the amino acid sequence Xac-Xad-Arg-Xaf-Xag, wherein Xac is an amino acid other than Glu, and Xad, Xaf and Xag are as defined in claim 13.

15. Labelled oligopeptide as a substrate for matrix metalloproteinase-13 activity, comprising the amino acid sequence Xal-Xam-Xan-Xao-Xap-Xaq, wherein Xal is any amino acid, preferably Pro or Hyp, Xam is a Arg, Lys, Orn, His or Trp, especially Arg, Xan is Gly, Ala, Abu or Val, especially Gly, Xao is any amino acid or a direct bond,
5 preferably Gly, Ala, Abu, Val, Nva, Leu, Nle or Ile, especially Leu, Xap is an amino acid capable of coupling to an amino group, preferably Asp, Aad or especially Glu, and Xaq is any amino acid, preferably Gly, Ala, Abu, Val, Nva, Leu, Nle or Ile, especially Ala.
16. Oligopeptide according to any one of claims 9-15, having a fluorescent label,
10 preferably also having a quenching group.
17. Labelled oligopeptide as a substrate for matrix metalloproteinase-1 (interstitial collagenase) activity, comprising the amino acid sequence Cha-Abu-Smc-His, preferably comprising the sequence Pro-Cha-Abu-Smc-His-Ala, to which a fluorescent label and a quenching group are bound.
- 15 18. Labelled oligopeptide as a substrate for matrix metalloproteinase-3 (stromelysin) activity, comprising the amino acid sequence Val-Glu-Nva-Trp, preferably comprising the sequence Pro-Val-Glu-Nva-Trp-Arg, to which Edans as a fluorescent label and Dabcyl as a quenching group are bound.
19. Oligopeptide according to any one of claims 9-18, bound, optionally in multiple
20 copies, to a water-insoluble carrier or protein.

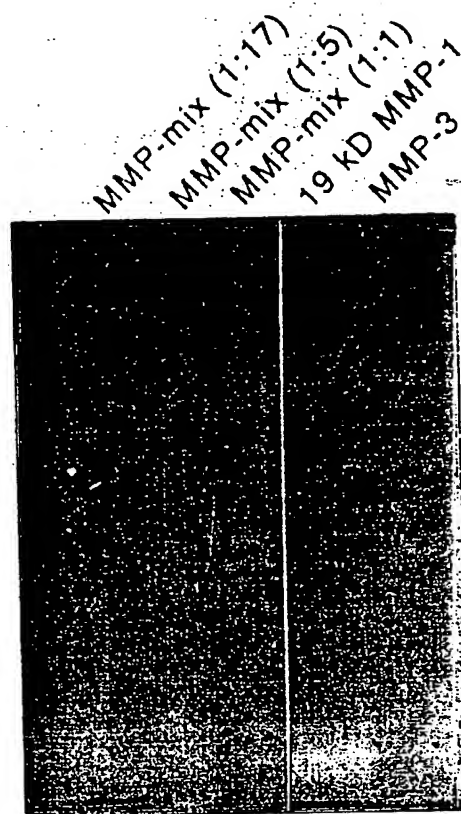
fig -1



fig-2



gelatin
zymography



fluorogenic
zymography

INTERNATIONAL SEARCH REPORT

International Application No.

PCT/NL 97/00002

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12Q1/37 C07K17/14 C07K7/04

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12Q C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	EP 0 428 000 A (ABBOTT LAB) 22 May 1991 cited in the application see the whole document ---	1,2,8
A	WO 91 16336 A (CARLSBERG AS) 31 October 1991 see abstract ---	1
A	EP 0 518 557 A (LILLY CO ELI) 16 December 1992 see abstract ---	1
A	WO 93 22429 A (SHRINERS HOSPITALS FOR CRIPPLE) 11 November 1993 see abstract ---	4
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☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
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Date of the actual completion of the international search

18 March 1997

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Ceder, O

INTERNATIONAL SEARCH REPORT

Int. Appl. No.

PCT/NL 97/00002

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

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A	GB 2 278 356 A (ZENECA LTD) 30 November 1994 see abstract ---	9,11
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Information on patent family members

Int. Appl. No.

PCT/NL 97/00002

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